Input file Fbh62112FL.seq; Output File 62112.trans
Sequence length 2452

```
                                                                          M   S   G     3
CGTGTGTGTGTGTCCCTGCGGCGCTAAGAAGGGGAGACTGAGGCTGAGGCTGGGGAACATCGGGCAGC ATG AGC GGC     9

   C   G   L   F   L   R   T   T   A   A   A   R   A   C   R   G   L   V   V   S    23
  TGC GGG CTC TTC CTG CGC ACC ACG GCT GCG GCT CGT GCC TGC CGG GGT CTG GTG GTC TCT    69

   T   A   N   R   R   L   L   R   T   S   P   P   V   R   A   F   A   K   E   L    43
  ACC GCG AAC CGG CGG CTA CTG CGC ACC AGC CCG CCT GTA CGA GCT TTC GCC AAA GAG CTT   129

   F   L   G   K   I   K   K   K   E   V   F   P   F   P   E   V   S   Q   D   E    63
  TTC CTA GGC AAA ATC AAG AAG AAA GAA GTT TTC CCA TTT CCA GAA GTT AGC CAA GAT GAA   189

   L   N   E   I   N   Q   F   L   G   P   V   E   K   F   F   T   E   E   V   D    83
  CTT AAT GAA ATC AAT CAG TTC TTG GGA CCC GTG GAA AAA TTC TTC ACT GAA GAG GTG GAC   249

   S   R   K   I   D   Q   E   G   K   I   P   D   E   T   L   E   K   L   K   S   103
  TCC CGA AAA ATT GAC CAG GAA GGG AAA ATC CCA GAT GAA ACT TTG GAG AAA TTG AAG AGC   309

   L   G   L   F   G   L   Q   V   P   E   E   Y   G   G   L   G   F   S   N   T   123
  CTA GGG CTT TTT GGG CTG CAA GTC CCA GAA GAA TAT GGT GGC CTG GGC TTC TCC AAC ACC   369

   M   Y   S   R   L   G   E   I   I   S   M   D   G   S   I   T   V   T   L   A   143
  ATG TAC TCA AGA CTA GGG GAG ATC ATC AGC ATG GAT GGG TCC ATC ACT GTG ACC CTG GCA   429

   A   H   Q   A   I   G   L   K   G   I   I   L   A   G   T   E   E   Q   K   A   163
  GCG CAC CAG GCT ATT GGC CTC AAG GGG ATC ATC TTG GCT GGC ACT GAG GAG CAG AAA GCC   489

   K   Y   L   P   K   L   A   S   G   E   H   I   A   A   F   C   L   T   E   P   183
  AAA TAC TTG CCT AAA CTG GCG TCC GGG GAG CAC ATT GCA GCC TTC TGC CTC ACG GAG CCA   549

   A   S   G   S   D   A   A   S   I   R   S   R   A   T   L   S   E   D   K   K   203
  GCC AGT GGG AGC GAT GCA GCC TCA ATC CGG AGC AGA GCC ACA CTA AGT GAA GAC AAG AAG   609

   H   Y   I   L   N   G   S   K   V   W   I   T   N   G   G   L   A   N   I   F   223
  CAC TAC ATC CTC AAT GGC TCC AAG GTC TGG ATT ACT AAT GGA GGA CTG GCC AAT ATT TTT   669

   T   V   F   A   K   T   E   V   V   D   S   D   G   S   V   K   D   K   I   T   243
  ACT GTG TTT GCA AAG ACT GAG GTC GTT GAT TCT GAT GGA TCA GTG AAA GAC AAA ATC ACA   729

   A   F   I   V   E   R   D   F   G   G   V   T   N   G   K   P   E   D   K   L   263
  GCA TTC ATA GTA GAA AGA GAC TTT GGT GGA GTC ACT AAT GGG AAA CCC GAA GAT AAA TTA   789

   G   I   R   G   S   N   T   C   E   V   H   F   E   N   T   K   I   P   V   E   283
  GGC ATT CGG GGC TCC AAC ACT TGT GAA GTC CAT TTT GAA AAC ACC AAG ATA CCT GTG GAA   849

   N   I   L   G   E   V   G   D   G   F   K   V   A   M   N   I   L   N   S   G   303
  AAC ATC CTT GGA GAG GTC GGA GAT GGG TTT AAG GTG GCC ATG AAC ATC CTC AAC AGC GGC   909

   R   F   S   M   G   S   V   V   A   G   L   L   K   R   L   I   E   M   T   A   323
  CGG TTC AGC ATG GGC AGC GTC GTG GCT GGG CTG CTC AAG AGA TTG ATT GAA ATG ACT GCT   969

   E   Y   A   C   T   R   K   Q   F   N   K   R   L   S   E   F   G   L   I   Q   343
  GAG TAC GCC TGC ACA AGG AAA CAG TTT AAC AAG AGG CTC AGT GAA TTT GGA TTG ATT CAG  1029

   E   K   F   A   L   M   A   Q   K   A   Y   V   M   E   S   M   T   Y   L   T   363
  GAG AAA TTT GCA CTG ATG GCT CAG AAG GCT TAC GTC ATG GAG AGT ATG ACC TAC CTC ACA  1089

   A   G   M   L   D   Q   P   G   F   P   D   C   S   I   E   A   A   M   V   K   383
  GCA GGG ATG CTG GAC CAA CCT GGC TTT CCC GAC TGC TCC ATC GAG GCA GCC ATG GTG AAG  1149
```

Fig. 1A

```
 V   F   S   S   E   A   A   W   Q   C   V   S   E   A   L   Q   I   L   G   G   403
GTG TTC AGC TCC GAG GCC GCC TGG CAG TGT GTG AGT GAG GCG CTG CAG ATC CTC GGG GGC 1209

 L   G   Y   T   R   D   Y   P   Y   E   R   I   L   R   D   T   R   I   L   L   423
TTG GGC TAC ACA AGG GAC TAT CCG TAC GAG CGC ATA CTG CGT GAC ACC CGC ATC CTC CTC 1269

 I   F   E   G   T   N   E   I   L   R   M   Y   I   A   L   T   G   L   Q   H   443
ATC TTC GAG GGA ACC AAT GAG ATT CTC CGG ATG TAC ATC GCC CTG ACG GGT CTG CAG CAT 1329

 A   G   R   I   L   T   T   R   I   H   E   L   K   Q   A   K   V   S   T   V   463
GCC GGC CGC ATC CTG ACT ACC AGG ATC CAT GAG CTT AAA CAG GCC AAA GTG AGC ACA GTC 1389

 M   D   T   V   G   R   R   L   R   D   S   L   G   R   T   V   D   L   G   L   483
ATG GAT ACC GTT GGC CGG AGG CTT CGG GAC TCC CTG GGC CGA ACT GTG GAC CTG GGG CTG 1449

 T   G   N   H   G   V   V   H   P   S   L   A   D   S   A   N   K   F   E   E   503
ACA GGC AAC CAT GGA GTT GTG CAC CCC AGT CTT GCG GAC AGT GCC AAC AAG TTT GAG GAG 1509

 N   T   Y   C   F   G   R   T   V   E   T   L   L   L   R   F   G   K   T   I   523
AAC ACC TAC TGC TTC GGC CGG ACC GTG GAG ACA CTG CTG CTC CGC TTT GGC AAG ACC ATC 1569

 M   E   E   Q   L   V   L   K   R   V   A   N   I   L   I   N   L   Y   G   M   543
ATG GAG GAG CAG CTG GTA CTG AAG CGG GTG GCC AAC ATC CTC ATC AAC CTG TAT GGC ATG 1629

 T   A   V   L   S   R   A   S   R   S   I   R   I   G   L   R   N   H   D   H   563
ACG GCC GTG CTG TCG CGG GCC AGC CGC TCC ATC CGC ATT GGG CTC CGC AAC CAC GAC CAC 1689

 E   V   L   L   A   N   T   F   C   V   E   A   Y   L   Q   N   L   F   S   L   583
GAG GTT CTC TTG GCC AAC ACC TTC TGC GTG GAA GCT TAC TTG CAG AAT CTC TTC AGC CTC 1749

 S   Q   L   D   K   Y   A   P   E   N   L   D   E   Q   I   K   K   V   S   Q   603
TCT CAG CTG GAC AAG TAT GCT CCA GAA AAC CTA GAT GAG CAG ATT AAG AAA GTG TCC CAG 1809

 Q   I   L   E   K   R   A   Y   I   C   A   H   P   L   D   R   T   C   *      622
CAG ATC CTT GAG AAG CGA GCC TAT ATC TGT GCC CAC CCT CTG GAC AGG ACA TGC TGA    1866
```

GGCAGGGGACAGTGTCCCCTGCTACCGCCCGCCCCTACCCATGGCCCGTTGCTGGATGACTGTTACTCTTTTTTCAGAA

GGTGTTGGGATTATCACAGGTTAAGCCTTTTGTTCCCCGTCTGCACCTGAAGGGTTGTCGCCTGGCCTGGGAGAGCCTC

TTCCAGGTTTTTGACCTGCAGGCAGTGCTCTCTAACAGGACCATCACAGCTTCTGAACTGAGCCGGAGAGAGAGAATGGA

ATTGCTGACCCCTGGAACTGGCGGGTATTCTGGTCATTGAGGAGACACCATAGTGGAAACTGGGGCTTATGCTGCTGCC

TCCAGGGTGTGAGGTGGGTGGGGACCTGTGTCAGGTGTGGATAGCCATTTCTGCTCAACCACACATTCTCTAAGAAACA

GCTTGAAAGCTCTGTCTGGGTCATTCATTTAAACTAGAAGCAGAGGCACTTAAAACATGTACCAGGAACCATTTAACAA

AGAATATAAAATGTCACAATCTGTGTACTGTTAAAAAAAAAAAAAA

Fig. 1B

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- -
HMM file: /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.26629.seq
- -
  Query: 62112

Scores for sequence family classification (score includes all domains):
Model   Description   Score   E-value N
--------   -----------   -----   ------- ---
Acyl-CoA_dh_M   Acyl-CoA dehydrogenase, middle domain 153.0   3.5e-42 1
Acyl-CoA_dh   Acyl-CoA dehydrogenase, C-terminal dom 152.1   9.6e-42 1
Acyl-CoA_dh_N   Acyl-CoA dehydrogenase, N-terminal dom   73.7   4.2e-19 1
Polysac_deacet   Polysaccharide deacetylase   -43.7   1.8   1

Parsed for domains:
Model   Domain seq-f seq-t'   hmm-f hmm-t   score   E-value
--------   ------- ----- -----   ----- -----   -----   -------
Acyl-CoA_dh_N   1/1   85   177 ..   29   132 .]   73.7   4.2e-19
Acyl-CoA_dh_M   1/1   179   286 ..   1   106 []   153.0   3.5e-42
Acyl-CoA_dh   1/1   290   441 ..   1   156 []   152.1   9.6e-42
Polysac_deacet   1/1   432   580 ..   1   150 []   -43.7   1.8

Alignments of top-scoring domains:
Acyl-CoA_dh_N: domain 1 of 1, from 85 to 177: score 73.7, E = 4.2e-19
               *->RRvDksgefPalrelikaLgqlGllginvPEeyGGaGad..ylaRFm
                  R++D++g+ P   e +++L lGl+g+ vPEeyGG+G +++ ++
      62112   85 RKIDQEGKIP--DETLEKLKSLGLFGLQVPEEYGGLGFSntMYS--- 126

                  LHAQVaalviEElarvcAstgvilsvhssLgqnpilkfGseEQKkkyLpq
                    + E+   ++s v+l++h ++g+ +i+ +G+eEQK+kyLp+
      62112 127 --------RLGEIISMDGSITVTLAAHQAIGLKGIILAGTEEQKAKYLPK 168

                  ltsGdliga<-*
                  l+sG++i+a
      62112 169 LASGEHIAA   177

Acyl-CoA_dh_M: domain 1 of 1, from 179 to 286: score 153.0, E = 3.5e-42
               *->AlTEPgAGSDvgSlkTtAekkEGd..dyiLNGsKmWITNGgqAdwyi
                  +lTEP +GSD++S++ +A+   d+++yiLNGsK+WITNGg A++++
      62112 179 CLTEPASGSDAASIRSRATLS-EDkkHYILNGSKVWITNGGLANIFT 224

                  VlAvT...DpakkvpgkkgitaFlVekdtpGfsiGkKedKLGlRgSdTcE
                  V+A+T+ D +   + k itaF+Ve+d+ G++ Gk+edKLG+RgS+TcE
      62112 225 VFAKTevvDSDG--SVKDKITAFIVERDFGGVINGKPEDKLGIRGSNICE 272

                  LiFEDvrvPesniL<-*
                  + FE+ ++P +niL
      62112 273 VHFENTKIPVENIL   286

Fig. 2A

Acyl-CoA_dh: domain 1 of 1, from 290 to 441: score 152.1, E = 9.6e-42
```
             *->GkGFkyamkeLdmeRlviAaqalGlaqgaldeAinYakqRkqFGkpl
                G+GFk+am+ L+ +R+  +++  Gl+ + ++ +++Ya  RkqF k+l
    62112   290  GDGFKVAMNILNSGRFSMGSVVAGLLKRLIEMTAEYACTRKQFNKRL 336


                adfQliQfkLAdMatkLEaaRllvYraAwladr.GedAKEALptskeaam
                +f liQ+k+A Ma k  ++ +++Y +A   d++G +     ++s eaam
    62112   337  SEFGLIQEKFALMAQKAYVMESMTYLTAGMLDQpGFP-----DCSIEAAM 381


                AKlfaseaAmqvatdAvQilGGvGYtkdyPveRfyRDAkitqIYEGTsEI
                +K f+seaA q +++A+QilGG GYt dyP eR +RD +i  I EGT+EI
    62112   382  VKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTRILLIFEGINEI 431


                qrlvIaRall<-*
                 r  Ia + l
    62112   432  LRMYIALTGL    441
```

Polysac_deacet: domain 1 of 1, from 432 to 580: score -43.7, E = 1.8
```
             *->ddksvyLTFDDGPnAApayTprlLDvLkkhkvkATFFviGsnvkdnP
                +++++LT + ++ +  T+r+ + Lk+ kv  +   G++ +d
    62112   432   LRMYIALTGLQHAG--RILTTRI-HELKQAKVSTVMDTVGRRLRD-- 473


                dlarrivkeGHeigNHtwsHPdlt.....................tl
                 + r v+ G  gNH+  HP l+++ ++ ++++   +++ ++ + +
    62112   474  -SLGRTVDLG-LTGNHGVVHPSLAdsankfeentycfgrtvetlllrfGK 521


                taeqirdeiertneaiiqatggatptlfRpPYGewsetvlsasaklGlaa
                t +++ + r+++++i+++g t++l R+     s+s ++Gl+
    62112   522  TIMEEQLVLKRVANILINLYG-MTAVLSRA---------SRSIRIGLRN 560


                vlWdvDprDWsvragadaivdavlqaa<-*
                +    D v  ++ v a+lq+
    62112   561  H-------DHEVLLANTFCVEAYLQNL    580
```

Fig. 2B

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- -
HMM file: /prod/ddm/seqanal/PFAM/pfam5.4/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.17193.seq
- -
  Query: 62112

Scores for sequence family classification (score includes all domains):
Model   Description   Score   E-value   N
--------   -----------   -----   -------   ---

Acyl-CoA_dh   Acyl-CoA dehydrogenase   399.8   1.8e-116   1
Polysac_deacet   Polysaccharide deacetylase   -43.7   1   1

Parsed for domains:
Model   Domain seq-f seq-t   hmm-f hmm-t   score   E-value
--------   ------- ----- -----   ----- -----   -----   -------

Acyl-CoA_dh   1/1   85   438 ..   29   394 .]   399.8 1.8e-116
Polysac_deacet   1/1   432   580 ..   1   150 []   -43.7   1

Alignments of top-scoring domains:
Acyl-CoA_dh: domain 1 of 1, from 85 to 438: score 399.8, E = 1.8e-116
              *->RRvDksgefPlrelikaLgklGllginvPEeyGGaGad..ylaRFmL
                 R++D++g+ P e +++L lGl+g+ vPEeyGG+G +++ ++
     62112   85   RKIDQEGKIP-DETLEKLKSLGLFGLQVPEEYGGLGFSntMYS---- 126

              HAQVaalviEElarvcAstgvllsvhssLgqnpilrfGseEQkkkyLpql
                 + E+   ++s v+l++h ++g+ i+ +G+eEQk+kyLp+l
     62112   127 -------RLGEIISMDGSITVTLAAHQAIGLKGIILAGTEEQKAKYLPKL 169

```
               tsGdligafAlTEPgAGSDvgSikTtAekkEGd..dyiLNGsKmWITNGg
               +sG++i+af+lTEP +GSD++Si+ +A+     d+++yiLNGsK+WITNGg
     62112  170 ASGEHIAAFCLTEPASGSDAASIRSRATLS-EDkkHYILNGSKVWITNGG 218


               qAdwyiVlAvT...DpakkvpgkkgitaFlVekdtpGfsiGkKedKLGlR
               A++++V+A+T+  D +   + k  itaF+Ve+d+ G++ Gk+edKLG+R
     62112  219 LANIFTVFAKTevvDSDG--SVKDKITAFIVERDFGGVTNGKPEDKLGIR 266


               gSdTcELiFEDvrvPesniLGeEGeGFkyaMktLdmeRlgiAaqalGiaq
               gS_TcE+ FE+ ++P +niLGe G+GFk+aM+ L+ +R+   +++  G++
     62112  267 GSNTCEVHFENTKIPVENILGEVGDGFKVAMNILNSGRFSMGSVVAGLLK 316


               gAldeAinYAkqRkqFGkplaefQliQfkLAdMAtkLEaaRllvYraAwl
               + ++ +++YA  RkqF k+l ef liQ+k+A MA k  ++ +++Y +A
     62112  317 RLIEMTAEYACTRKQFNKRLSEFGLIQEKFALMAQKAYVMESMTYLTAGM 366


               adr.GedAKEALptskeAAMAKlfAseiAmkvatdAvQilGGvGYtkdyP
               d++G +      ++s eAAM+K f+se+A + +++A+QilGG GYt dyP
     62112  367 LDQpGFP-----DCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYP 411


               veRfyRDAkitqIYEGTsEIQrlvIaR<-*
               eR +RD +i  I EGT+EI r  Ia
     62112  412 YERILRDTRILLIFEGTNEILRMYIAL      438


Polysac_deacet: domain 1 of 1, from 432 to 580: score -43.7, E = 1
               *->ddksvyLTFDDGPnAApayTprlLDvLkkhkvkATFFviGsnvkdnP
                  +++++LT + ++  +  T+r+ + Lk+ kv  +   G++ +d
     62112  432    LRMYIALTGLQHAG--RILTTRI-HELKQAKVSTVMDTVGRRLRD-- 473


               dlarrivkeGHeigNHtwsHPdlt.................tl
               + r v+ G  gNH+  HP l+++ ++ ++++  +++ ++  + +
     62112  474 -SLGRTVDLG-LTGNHGVVHPSLAdsankfeentycfgrtvetlllrfGK 521


               taeqirdeiertneaiiqatggatptlfRpPYGewsetvlsasaklGlta
               t +++  + r+++++i+++g  t++l R+        s+s ++Gl+
     62112  522 TIMEEQLVLKRVANILINLYG-MTAVLSRA---------SRSIRIGLRN 560


               vlWdvDprDWsvragadaivdavlqaa<-*
               +      D v ++ v a+lq+
     62112  561 H-------DHEVLLANTFCVEAYLQNL     580
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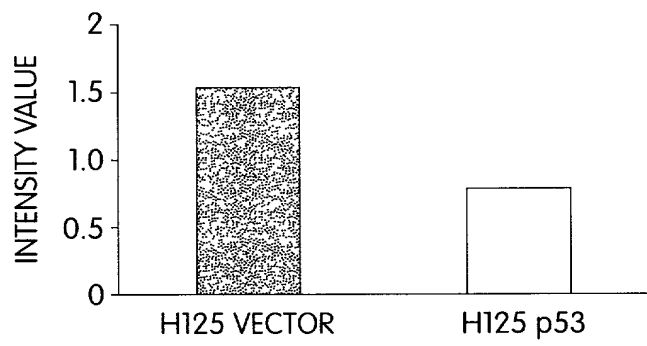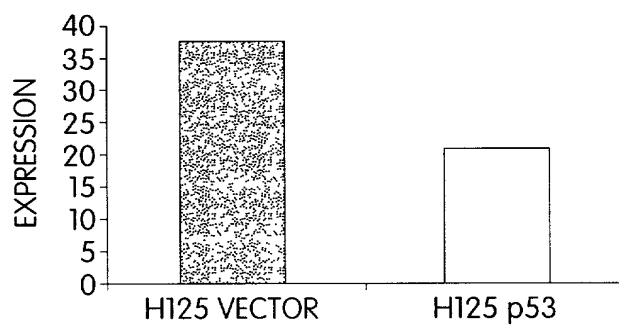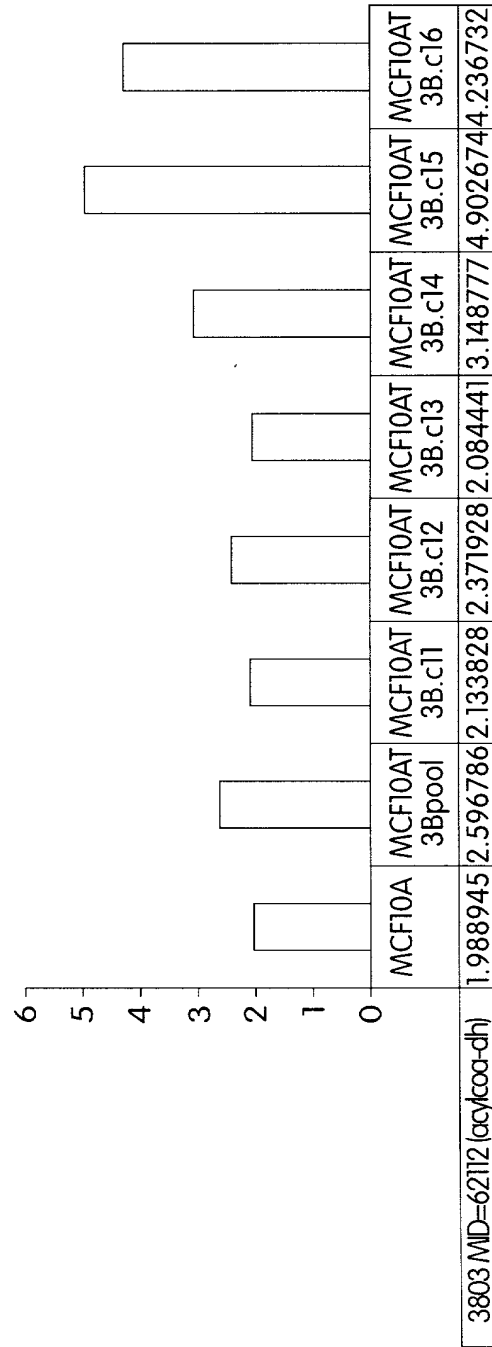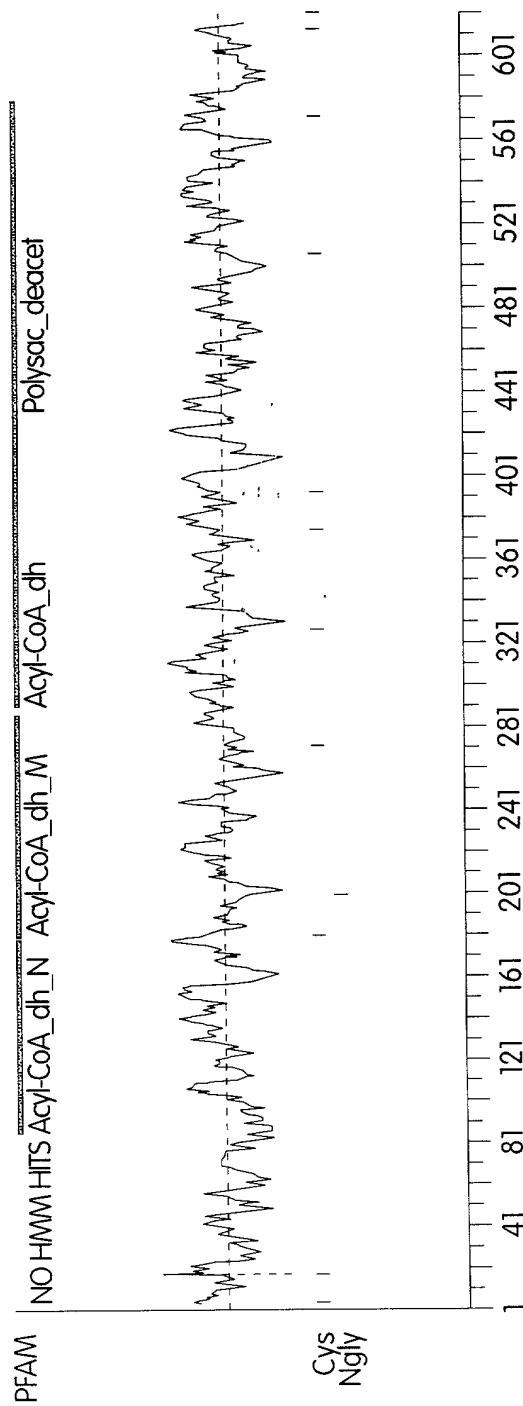
Fig. 2D

Fig. 3A

Fig. 3B

	MCF10A	MCF10AT 3Bpool	MCF10AT 3B.cl1	MCF10AT 3B.cl2	MCF10AT 3B.cl3	MCF10AT 3B.cl4	MCF10AT 3B.cl5	MCF10AT 3B.cl6
3803 MID=62112 (acylcoa-dh)	1.988945	2.596786	2.133828	2.371928	2.084441	3.148777	4.902674	4.236732

Fig. 4

Fig. 5